

In the Specification:

Please replace the last paragraph at the bottom of page 1 (which wraps around to the top of page 2) with the following paragraph:

Transporters are generally classified by structure and the type of mode of action. In addition, transporters are sometimes classified by the molecule type that is transported, for example, sugar transporters, chlorine channels, potassium channels, etc. There may be many classes of channels for transporting a single type of molecule (a detailed review of channel types can be found at Alexander, S.P.H. and J.A. Peters: Receptor and transporter nomenclature supplement. Trends Pharmacol. Sci., Elsevier, pp. 65-68 (1997) ~~and <http://www-biology.ucsd.edu/~msaier/transport/titlepage2.html>~~.

Please replace the last paragraph on page 4 (which wraps around to the top of page 5) with the following paragraph:

Ion channels are generally classified by structure and the type of mode of action. For example, extracellular ligand gated channels (ELGs) are comprised of five polypeptide subunits, with each subunit having 4 membrane spanning domains, and are activated by the binding of an extracellular ligand to the channel. In addition, channels are sometimes classified by the ion type that is transported, for example, chlorine channels, potassium channels, etc. There may be many classes of channels for transporting a single type of ion (a detailed review of channel types can be found at Alexander, S.P.H. and J.A. Peters (1997). Receptor and ion channel nomenclature supplement. Trends Pharmacol. Sci., Elsevier, pp. 65-68 ~~and <http://www-biology.ucsd.edu/~msaier/transport/toc.html>~~.

Please replace the second paragraph at the bottom of page 21 with the following paragraph:

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and

Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (~~available at <http://www.gcg.com>~~), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al.*, *Nucleic Acids Res.* 12(1):387 (1984)) (~~available at <http://www.gcg.com>~~), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

Please replace Section “DESCRIPTION OF THE FIGURE SHEETS” on page 15 with the following paragraph

DESCRIPTION OF THE FIGURE SHEETS

FIGURES 1A-1B provides the nucleotide sequence of a cDNA molecule or transcript sequence that encodes the transporter protein of the present invention (SEQ ID NO:1). In addition structure and functional information is provided, such as ATG start, stop and tissue distribution, where available, that allows one to readily determine specific uses of inventions based on this molecular sequence. Experimental data as provided in Figure 1 indicates expression in humans in brain, heart, kidney, lung, spleen, testis, leukocyte and fetal brain.

FIGURES 2A-2D provides the predicted amino acid sequence of the transporter of the present invention. (SEQ ID NO: 2) In addition structure and functional information such as protein family, function, and modification sites is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence.

FIGURES 3A-3MMM provides genomic sequences that span the gene encoding the transporter protein of the present invention (SEQ ID NO: 3). In addition structure and functional information, such as intron/exon structure, promoter location, etc., is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence. 140 SNPs, including 6 indels, have been identified in the gene encoding the transporter protein provided by the present invention and are given in Figure 3.